

# SEQUENCE LISTING

<110> Vuolteenaho, Olli  
Ala-Kopsala, Minna  
Ruskoaho, Heikki  
Leppaluoto, Juhani  
Haapalahti, Jouko

<120> Assay

<130> 50318/011001

<140> US 10/562,081

<141> 2005-12-23

<150> PCT/EP2004/006971

<151> 2004-06-28

<150> GB 0315291.5

<151> 2003-06-30

<160> 36

<170> PatentIn version 3.3

<210> 1

<211> 126

<212> PRT

<213> Homo sapiens

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Val	Pro	Pro	Gln	Val	Leu	Ser	Glu	Pro	Asn	Glu	Glu	Ala	Gly	Ala	Ala
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Ala	Gln	Arg	Asp	Gly	Gly	Ala	Leu	Gly	Arg	Gly	Pro	Trp	Asp	Ser	Ser
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Asp	Arg	Ser	Ala	Leu	Leu	Lys	Ser	Lys	Leu	Arg	Ala	Leu	Leu	Thr	Ala
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Pro	Arg	Ser	Leu	Arg	Arg	Ser	Ser	Cys	Phe	Gly	Gly	Arg	Met	Asp	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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 20 25 30  
  
 Val Pro Pro Gln Val Leu Ser Glu Pro Asn Glu Glu Ala Gly Ala Ala  
 35 40 45  
  
 Leu Ser Pro Leu Pro Glu Val Pro Pro Trp Thr Gly Glu Val Ser Pro  
 50 55 60  
  
 Ala Gln Arg Asp Gly Gly Ala Leu Gly Arg Gly Pro Trp Asp Ser Ser  
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 Pro Arg

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His Pro Leu Gly Ser Pro Gly Ser Ala Ser Asp Leu Glu Thr Ser Gly  
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Leu Gln Glu Gln Arg Asn His Leu Gln Gly Lys Leu Ser Glu Leu Gln  
 20 25 30

Val Glu Gln Thr Ser Leu Glu Pro Leu Gln Glu Ser Pro Arg Pro Thr  
 35 40 45

Gly Val Trp Lys Ser Arg Glu Val Ala Thr Glu Gly Ile Arg Gly His  
 50 55 60

Arg Lys Met Val Leu Tyr Thr Leu Arg Ala Pro Arg Ser Pro Lys Met  
 65 70 75 80

Val Gln Gly Ser Gly Cys Phe Gly Arg Lys Met Asp Arg Ile Ser Ser  
 85 90 95

Ser Ser Gly Leu Gly Cys Lys Val Leu Arg Arg His  
 100 105

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 <213> Homo sapiens

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 20 25 30

Val Glu Gln Thr Ser Leu Glu Pro Leu Gln Glu Ser Pro Arg Pro Thr  
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Gly Val Trp Lys Ser Arg Glu Val Ala Thr Glu Gly Ile Arg Gly His  
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Arg Lys Met Val Leu Tyr Thr Leu Arg Ala Pro Arg  
 65 70 75

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 120

ccgaatgaag aagcgggggc tgctctcagc cccctccctg aggtgcctcc ctggaccggg  
 180

gaagtcagcc cagcccagag agatggaggt gccctcgggc ggggccctg ggactcctct  
 240

gatcgatctg cctcctaaa aagcaagctg agggcgctgc tactgcccc tcggagcctg  
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 360

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120

ccgaatgaag aagcgggggc tgctctcagc cccctccctg aggtgcctcc ctggaccggg  
180

gaagtcagcc cagcccagag agatggaggt gccctcgggc ggggccctg ggactcctct  
240

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294

<210> 10  
<211> 324  
<212> DNA  
<213> Homo sapiens

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ctccaggaga gccccgtcc cacaggtgtc tggaagtccc gggaggtagc caccgagggc  
180

atccgtgggc accgcaaaat ggtcctctac accctgcggg caccacgaag cccaagatg  
240

gtgcaagggt ctggctgctt tgggaggaag atggaccgga tcagctctc cagtggcctg  
300

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324

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<212> DNA  
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tccagtggcc tgggctgcaa agtgctgagg cggcat  
96

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ctccaggaga gccccgtcc cacagggtgc tggaagtccc gggaggtagc caccgagggc  
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<220>  
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<400> 14

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20 25 30

Val Glu Gln Thr Ser Glu Asp Glu Val Val Pro Pro Gln Val Leu Ser  
35 40 45

Glu Pro Asn Glu Glu Ala Gly Ala Ala Leu Ser Pro Leu Pro Glu Val  
50 55 60

Pro Pro Trp Thr Gly Glu Val Ser Pro Ala Gln Arg Asp Gly Gly Ala  
65 70 75 80

Leu Gly Arg Gly Pro Trp Asp Ser Ser Asp Arg Ser Ala Leu Leu Lys  
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Ser Lys Leu Arg Ala Leu Leu Thr Ala Pro Arg  
100 105

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1 5 10 15

Gly Lys Leu Ser Asp His Leu Glu Glu Lys Met Pro Leu Glu Asp Glu  
20 25 30

Val Val Pro Pro Gln Val Leu Ser Glu Pro Asn Glu Glu Ala Gly Ala  
35 40 45

Ala Leu Ser Pro Leu Pro Glu Val Pro Pro Trp Thr Gly Glu Val Ser  
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Ser

<210> 16  
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 <223> Synthetic peptide

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<210> 17  
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 <212> PRT  
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<400> 17

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Leu Gln Glu Gln Arg Asn His Leu Gln Gly Lys Leu Ser Glu Leu Gln  
 20 25 30

Val Glu Gln Thr Ser Leu Glu Pro Leu Gln Glu Ser Pro Arg Pro Thr  
 35 40 45

Gly Val Trp Lys Ser Arg Glu Val Ala Thr Glu Gly Ile Arg Gly His  
 50 55 60

Arg Lys Met Val Leu Tyr Thr Leu Arg Ala Pro Arg Asn Pro Met Tyr  
 65 70 75 80

Asn Ala Val Ser Asn Ala Asp Leu Met Asp Phe Lys Asn Leu Leu Asp  
 85 90 95

His Leu Glu Glu Lys Met Pro Leu Glu Asp Glu Val Val Pro Pro Gln  
 100 105 110

Val Leu Ser Glu Pro Asn Glu Glu Ala Gly Ala Ala Leu Ser Pro Leu  
 115 120 125



Pro Glu Val Pro Pro Trp Thr Gly Glu Val Ser Pro Ala Gln Arg Asp  
130 135 140

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145 150 155 160

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<210> 18  
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<400> 18

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Gly Lys Leu Ser Gly Glu Val Ser Pro Ala Gln Arg Asp Gly Gly Ala  
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Leu Gly Arg Gly Pro Trp Asp Ser Ser  
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<210> 19  
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Leu Gln Glu Gln Arg Asn His Leu Gln Gly Lys Leu Ser Glu Leu Gln  
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Val Glu Gln Thr Ser Leu Glu Pro Leu Gln Glu Ser Pro Arg Pro Thr  
35 40 45

Gly Val Trp Lys Ser Arg Glu Val Ala Thr Glu Gly Ile Arg Gly His  
 50 55 60

Arg Lys Met Val Leu Tyr Thr Leu Arg Ala Pro Arg Ser Pro Lys Met  
 65 70 75 80

Val Gln Gly Ser Gly Cys Phe Gly Arg Lys Met Asp Arg Ile Ser Ser  
 85 90 95

Ser Ser Gly Leu Gly Cys Lys Val Leu Arg Arg His Asn Pro Met Tyr  
 100 105 110

Asn Ala Val Ser Asn Ala Asp Leu Met Asp Phe Lys Asn Leu Leu Asp  
 115 120 125

His Leu Glu Glu Lys Met Pro Leu Glu Asp Glu Val Val Pro Pro Gln  
 130 135 140

Val Leu Ser Glu Pro Asn Glu Glu Ala Gly Ala Ala Leu Ser Pro Leu  
 145 150 155 160

Pro Glu Val Pro Pro Trp Thr Gly Glu Val Ser Pro Ala Gln Arg Asp  
 165 170 175

Gly Gly Ala Leu Gly Arg Gly Pro Trp Asp Ser Ser Asp Arg Ser Ala  
 180 185 190

Leu Leu Lys Ser Lys Leu Arg Ala Leu Leu Thr Ala Pro Arg Ser Leu  
 195 200 205

Arg Arg Ser Ser Cys Phe Gly Gly Arg Met Asp Arg Ile Gly Ala Gln  
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Ser Gly Leu Gly Cys Asn Ser Phe Arg Tyr  
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<210> 20  
 <211> 31  
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 <213> Artificial sequence

<220>  
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Arg Ile Gly Ala Gln Ser Gly Leu Gly Cys Asn Ser Phe Arg Tyr  
 20 25 30

<210> 21  
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 <212> DNA  
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 cgcaaccatt tgcagggcaa actgtcggag ctgcaggtgg agcagacatc cgaagatgag  
 120  
 gtcgtgcccc cacaagtgct cagtgagccg aatgaagaag cgggggctgc tctcagcccc  
 180  
 ctccctgagg tgctccctg gaccggggaa gtcagcccag ccagagaga tggaggtgcc  
 240  
 ctcgggcggg gccctggga ctctctgat cgatctgccc tcctaaaaag caagctgagg  
 300  
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<210> 23  
 <211> 241  
 <212> DNA  
 <213> Artificial sequence

<220>

<223> Synthetic nucleic acid

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ccatttgga gaaaagatgc ctttagaaga tgaggctcgtg cccccacaag tgctcagtga  
120

gccgaatgaa gaagcggggg ctgctctcag cccctccct gaggtgcctc cctggaccgg  
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ggaagtcagc ccagcccaga gagatggagg tgccctcggg cggggccctt gggactcctc  
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241

<210> 24

<211> 522

<212> DNA

<213> Artificial sequence

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<223> Synthetic nucleic acid

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120

ctccaggaga gccccgtcc cacaggtgtc tggaagtccc gggaggtagc caccgagggc  
180

atccgtgggc accgcaaaat ggtcctctac accctgcggg caccacgaaa tcccatgtac  
240

aatgccgtgt ccaacgcaga cctgatggat ttcaagaatt tgctggacca tttggaagaa  
300

aagatgcctt tagaagatga ggtcgtgccc ccacaagtgc tcagttagcc gaatgaagaa  
360

gcgggggctg ctctcagccc cctccctgag gtgcctccct ggaccgggga agtcagccca  
420

gccagagag atggaggtgc cctcgggcgg ggccctggg actcctctga tcgatctgcc  
480

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<220>  
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<210> 26  
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 ctccaggaga gccccgtcc cacaggtgtc tggaagtccc gggaggtagc caccgagggc  
 180  
  
 atccgtgggc accgcaaaat ggtcctctac accctgcggg caccacgaag cccaagatg  
 240  
  
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 300  
  
 ggctgcaaag tgctgaggcg gcataatccc atgtacaatg ccgtgtccaa cgcagacctg  
 360  
  
 atggatttca agaatttgct ggaccatttg gaagaaaaga tgcctttaga agatgaggtc  
 420  
  
 gtgccccac aagtgtcag tgagccgaat gaagaagcgg gggctgctct cagccccctc  
 480  
  
 cctgaggtgc ctccctggac cggggaagtc agcccagccc agagagatgg aggtgccttc  
 540

gggcggggcc cctgggactc ctctgatcga tctgccctcc taaaaagcaa gctgagggcg  
600

ctgctcactg cccctcggag cctgcggaga tccagctgct tcgggggcag gatggacagg  
660

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93

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<212> DNA  
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<220>  
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<400> 29  
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<210>  31
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<223>  Primer

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<223>  Primer

<400>  32
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25

<210>  33
<211>  1061
<212>  PRT
<213>  Homo sapiens

<400>  33

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20          25          30

Gly  Asn  Leu  Thr  Val  Ala  Val  Val  Leu  Pro  Leu  Ala  Asn  Thr  Ser  Tyr
35          40          45

Pro  Trp  Ser  Trp  Ala  Arg  Val  Gly  Pro  Ala  Val  Glu  Leu  Ala  Leu  Ala
50          55          60

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Gln Val Lys Ala Arg Pro Asp Leu Leu Pro Gly Trp Thr Val Arg Thr  
 65 70 75 80

Val Leu Gly Ser Ser Glu Asn Ala Leu Gly Val Cys Ser Asp Thr Ala  
 85 90 95

Ala Pro Leu Ala Ala Val Asp Leu Lys Trp Glu His Asn Pro Ala Val  
 100 105 110

Phe Leu Gly Pro Gly Cys Val Tyr Ala Ala Ala Pro Val Gly Arg Phe  
 115 120 125

Thr Ala His Trp Arg Val Pro Leu Leu Thr Ala Gly Ala Pro Ala Leu  
 130 135 140

Gly Phe Gly Val Lys Asp Glu Tyr Ala Leu Thr Thr Arg Ala Gly Pro  
 145 150 155 160

Ser Tyr Ala Lys Leu Gly Asp Phe Val Ala Ala Leu His Arg Arg Leu  
 165 170 175

Gly Trp Glu Arg Gln Ala Leu Met Leu Tyr Ala Tyr Arg Pro Gly Asp  
 180 185 190

Glu Glu His Cys Phe Phe Leu Val Glu Gly Leu Phe Met Arg Val Arg  
 195 200 205

Asp Arg Leu Asn Ile Thr Val Asp His Leu Glu Phe Ala Glu Asp Asp  
 210 215 220

Leu Ser His Tyr Thr Arg Leu Leu Arg Thr Met Pro Arg Lys Gly Arg  
 225 230 235 240

Val Ile Tyr Ile Cys Ser Ser Pro Asp Ala Phe Arg Thr Leu Met Leu  
 245 250 255

Leu Ala Leu Glu Ala Gly Leu Cys Gly Glu Asp Tyr Val Phe Phe His  
 260 265 270

Leu Asp Ile Phe Gly Gln Ser Leu Gln Gly Gly Gln Gly Pro Ala Pro  
 275 280 285

Arg Arg Pro Trp Glu Arg Gly Asp Gly Gln Asp Val Ser Ala Arg Gln



290		295		300
Ala Phe Gln Ala Ala Lys Ile Ile Thr Tyr Lys Asp Pro Asp Asn Pro				
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Glu Tyr Leu Glu Phe Leu Lys Gln Leu Lys His Leu Ala Tyr Glu Gln				
	325		330	335
Phe Asn Phe Thr Met Glu Asp Gly Leu Val Asn Thr Ile Pro Ala Ser				
	340		345	350
Phe His Asp Gly Leu Leu Leu Tyr Ile Gln Ala Val Thr Glu Thr Leu				
	355		360	365
Ala His Gly Gly Thr Val Thr Asp Gly Glu Asn Ile Thr Gln Arg Met				
	370		375	380
Trp Asn Arg Ser Phe Gln Gly Val Thr Gly Tyr Leu Lys Ile Asp Ser				
385		390		395 400
Ser Gly Asp Arg Glu Thr Asp Phe Ser Leu Trp Asp Met Asp Pro Glu				
	405		410	415
Asn Gly Ala Phe Arg Val Val Leu Asn Tyr Asn Gly Thr Ser Gln Glu				
	420		425	430
Leu Val Ala Val Ser Gly Arg Lys Leu Asn Trp Pro Leu Gly Tyr Pro				
	435		440	445
Pro Pro Asp Ile Pro Lys Cys Gly Phe Asp Asn Glu Asp Pro Ala Cys				
	450		455	460
Asn Gln Asp His Leu Ser Thr Leu Glu Val Leu Ala Leu Val Gly Ser				
465		470		475 480
Leu Ser Leu Leu Gly Ile Leu Ile Val Ser Phe Phe Ile Tyr Arg Lys				
	485		490	495
Met Gln Leu Glu Lys Glu Leu Ala Ser Glu Leu Trp Arg Val Arg Trp				
	500		505	510
Glu Asp Val Glu Pro Ser Ser Leu Glu Arg His Leu Arg Ser Ala Gly				
	515		520	525

Ser Arg Leu Thr Leu Ser Gly Arg Gly Ser Asn Tyr Gly Ser Leu Leu  
 530 535 540

Thr Thr Glu Gly Gln Phe Gln Val Phe Ala Lys Thr Ala Tyr Tyr Lys  
 545 550 555 560

Gly Asn Leu Val Ala Val Lys Arg Val Asn Arg Lys Arg Ile Glu Leu  
 565 570 575

Thr Arg Lys Val Leu Phe Glu Leu Lys His Met Arg Asp Val Gln Asn  
 580 585 590

Glu His Leu Thr Arg Phe Val Gly Ala Cys Thr Asp Pro Pro Asn Ile  
 595 600 605

Cys Ile Leu Thr Glu Tyr Cys Pro Arg Gly Ser Leu Gln Asp Ile Leu  
 610 615 620

Glu Asn Glu Ser Ile Thr Leu Asp Trp Met Phe Arg Tyr Ser Leu Thr  
 625 630 635 640

Asn Asp Ile Val Lys Gly Met Leu Phe Leu His Asn Gly Ala Ile Cys  
 645 650 655

Ser His Gly Asn Leu Lys Ser Ser Asn Cys Val Val Asp Gly Arg Phe  
 660 665 670

Val Leu Lys Ile Thr Asp Tyr Gly Leu Glu Ser Phe Arg Asp Leu Asp  
 675 680 685

Pro Glu Gln Gly His Thr Val Tyr Ala Lys Lys Leu Trp Thr Ala Pro  
 690 695 700

Glu Leu Leu Arg Met Ala Ser Pro Pro Val Arg Gly Ser Gln Ala Gly  
 705 710 715 720

Asp Val Tyr Ser Phe Gly Ile Ile Leu Gln Glu Ile Ala Leu Arg Ser  
 725 730 735

Gly Val Phe His Val Glu Gly Leu Asp Leu Ser Pro Lys Glu Ile Ile  
 740 745 750

Glu Arg Val Thr Arg Gly Glu Gln Pro Pro Phe Arg Pro Ser Leu Ala  
755 760 765

Leu Gln Ser His Leu Glu Glu Leu Gly Leu Leu Met Gln Arg Cys Trp  
770 775 780

Ala Glu Asp Pro Gln Glu Arg Pro Pro Phe Gln Gln Ile Arg Leu Thr  
785 790 795 800

Leu Arg Lys Phe Asn Arg Glu Asn Ser Ser Asn Ile Leu Asp Asn Leu  
805 810 815

Leu Ser Arg Met Glu Gln Tyr Ala Asn Asn Leu Glu Glu Leu Val Glu  
820 825 830

Glu Arg Thr Gln Ala Tyr Leu Glu Glu Lys Arg Lys Ala Glu Ala Leu  
835 840 845

Leu Tyr Gln Ile Leu Pro His Ser Val Ala Glu Gln Leu Lys Arg Gly  
850 855 860

Glu Thr Val Gln Ala Glu Ala Phe Asp Ser Val Thr Ile Tyr Phe Ser  
865 870 875 880

Asp Ile Val Gly Phe Thr Ala Leu Ser Ala Glu Ser Thr Pro Met Gln  
885 890 895

Val Val Thr Leu Leu Asn Asp Leu Tyr Thr Cys Phe Asp Ala Val Ile  
900 905 910

Asp Asn Phe Asp Val Tyr Lys Val Glu Thr Ile Gly Asp Ala Tyr Met  
915 920 925

Val Val Ser Gly Leu Pro Val Arg Asn Gly Arg Leu His Ala Cys Glu  
930 935 940

Val Ala Arg Met Ala Leu Ala Leu Leu Asp Ala Val Arg Ser Phe Arg  
945 950 955 960

Ile Arg His Arg Pro Gln Glu Gln Leu Arg Leu Arg Ile Gly Ile His  
965 970 975

Thr Gly Pro Val Cys Ala Gly Val Val Gly Leu Lys Met Pro Arg Tyr  
980 985 990

Cys Leu Phe Gly Asp Thr Val Asn Thr Ala Ser Arg Met Glu Ser Asn  
995 1000 1005

Gly Glu Ala Leu Lys Ile His Leu Ser Ser Glu Thr Lys Ala Val  
1010 1015 1020

Leu Glu Glu Phe Gly Gly Phe Glu Leu Glu Leu Arg Gly Asp Val  
1025 1030 1035

Glu Met Lys Gly Lys Gly Lys Val Arg Thr Tyr Trp Leu Leu Gly  
1040 1045 1050

Glu Arg Gly Ser Ser Thr Arg Gly  
1055 1060

<210> 34  
<211> 430  
<212> PRT  
<213> Homo sapiens

<400> 34

Gly Asn Leu Thr Val Ala Val Val Leu Pro Leu Ala Asn Thr Ser Tyr  
1 5 10 15

Pro Trp Ser Trp Ala Arg Val Gly Pro Ala Val Glu Leu Ala Leu Ala  
20 25 30

Gln Val Lys Ala Arg Pro Asp Leu Leu Pro Gly Trp Thr Val Arg Thr  
35 40 45

Val Leu Gly Ser Ser Glu Asn Ala Leu Gly Val Cys Ser Asp Thr Ala  
50 55 60

Ala Pro Leu Ala Ala Val Asp Leu Lys Trp Glu His Asn Pro Ala Val  
65 70 75 80

Phe Leu Gly Pro Gly Cys Val Tyr Ala Ala Ala Pro Val Gly Arg Phe  
85 90 95

Thr Ala His Trp Arg Val Pro Leu Leu Thr Ala Gly Ala Pro Ala Leu  
100 105 110

Gly Phe Gly Val Lys Asp Glu Tyr Ala Leu Thr Thr Arg Ala Gly Pro  
 115 120 125

Ser Tyr Ala Lys Leu Gly Asp Phe Val Ala Ala Leu His Arg Arg Leu  
 130 135 140

Gly Trp Glu Arg Gln Ala Leu Met Leu Tyr Ala Tyr Arg Pro Gly Asp  
 145 150 155 160

Glu Glu His Cys Phe Phe Leu Val Glu Gly Leu Phe Met Arg Val Arg  
 165 170 175

Asp Arg Leu Asn Ile Thr Val Asp His Leu Glu Phe Ala Glu Asp Asp  
 180 185 190

Leu Ser His Tyr Thr Arg Leu Leu Arg Thr Met Pro Arg Lys Gly Arg  
 195 200 205

Val Ile Tyr Ile Cys Ser Ser Pro Asp Ala Phe Arg Thr Leu Met Leu  
 210 215 220

Leu Ala Leu Glu Ala Gly Leu Cys Gly Glu Asp Tyr Val Phe Phe His  
 225 230 235 240

Leu Asp Ile Phe Gly Gln Ser Leu Gln Gly Gly Gln Gly Pro Ala Pro  
 245 250 255

Arg Arg Pro Trp Glu Arg Gly Asp Gly Gln Asp Val Ser Ala Arg Gln  
 260 265 270

Ala Phe Gln Ala Ala Lys Ile Ile Thr Tyr Lys Asp Pro Asp Asn Pro  
 275 280 285

Glu Tyr Leu Glu Phe Leu Lys Gln Leu Lys His Leu Ala Tyr Glu Gln  
 290 295 300

Phe Asn Phe Thr Met Glu Asp Gly Leu Val Asn Thr Ile Pro Ala Ser  
 305 310 315 320

Phe His Asp Gly Leu Leu Leu Tyr Ile Gln Ala Val Thr Glu Thr Leu  
 325 330 335

Ala His Gly Gly Thr Val Thr Asp Gly Glu Asn Ile Thr Gln Arg Met  
 340 345 350

Trp Asn Arg Ser Phe Gln Gly Val Thr Gly Tyr Leu Lys Ile Asp Ser  
 355 360 365

Ser Gly Asp Arg Glu Thr Asp Phe Ser Leu Trp Asp Met Asp Pro Glu  
 370 375 380

Asn Gly Ala Phe Arg Val Val Leu Asn Tyr Asn Gly Thr Ser Gln Glu  
 385 390 395 400

Leu Val Ala Val Ser Gly Arg Lys Leu Asn Trp Pro Leu Gly Tyr Pro  
 405 410 415

Pro Pro Asp Ile Pro Lys Cys Gly Phe Asp Asn Glu Asp Pro  
 420 425 430

<210> 35  
 <211> 1047  
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 <213> Homo sapiens

<400> 35

Met Ala Leu Pro Ser Leu Leu Leu Leu Val Ala Ala Leu Ala Gly Gly  
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Val Arg Pro Pro Gly Ala Arg Asn Leu Thr Leu Ala Val Val Leu Pro  
 20 25 30

Glu His Asn Leu Ser Tyr Ala Trp Ala Trp Pro Arg Val Gly Pro Ala  
 35 40 45

Val Ala Leu Ala Val Glu Ala Leu Gly Arg Ala Leu Pro Val Asp Leu  
 50 55 60

Arg Phe Val Ser Ser Glu Leu Glu Gly Ala Cys Ser Glu Tyr Leu Ala  
 65 70 75 80

Pro Leu Ser Ala Val Asp Leu Lys Leu Tyr His Asp Pro Asp Leu Leu  
 85 90 95

Leu Gly Pro Gly Cys Val Tyr Pro Ala Ala Ser Val Ala Arg Phe Ala



Phe Tyr Asp Gly Ile Leu Leu Tyr Ala Glu Val Leu Asn Glu Thr Ile  
340 345 350

Gln Glu Gly Gly Thr Arg Glu Asp Gly Leu Arg Ile Val Glu Lys Met  
355 360 365

Gln Gly Arg Arg Tyr His Gly Val Thr Gly Leu Val Val Met Asp Lys  
370 375 380

Asn Asn Asp Arg Glu Thr Asp Phe Val Leu Trp Ala Met Gly Asp Leu  
385 390 395 400

Asp Ser Gly Asp Phe Gln Pro Ala Ala His Tyr Ser Gly Ala Glu Lys  
405 410 415

Gln Ile Trp Trp Thr Gly Arg Pro Ile Pro Trp Val Lys Gly Ala Pro  
420 425 430

Pro Ser Asp Asn Pro Pro Cys Ala Phe Asp Leu Asp Asp Pro Ser Cys  
435 440 445

Asp Lys Thr Pro Leu Ser Thr Leu Ala Ile Val Ala Leu Gly Thr Gly  
450 455 460

Ile Thr Phe Ile Met Phe Gly Val Ser Ser Phe Leu Ile Phe Arg Lys  
465 470 475 480

Leu Met Leu Glu Lys Glu Leu Ala Ser Met Leu Trp Arg Ile Arg Trp  
485 490 495

Glu Glu Leu Gln Phe Gly Asn Ser Glu Arg Tyr His Lys Gly Ala Gly  
500 505 510

Ser Arg Leu Thr Leu Ser Leu Arg Gly Ser Ser Tyr Gly Ser Leu Met  
515 520 525

Thr Ala His Gly Lys Tyr Gln Ile Phe Ala Asn Thr Gly His Phe Lys  
530 535 540

Gly Asn Val Val Ala Ile Lys His Val Asn Lys Lys Arg Ile Glu Leu  
545 550 555 560



Thr Arg Gln Val Leu Phe Glu Leu Lys His Met Arg Asp Val Gln Phe  
 565 570 575

Asn His Leu Thr Arg Phe Ile Gly Ala Cys Ile Asp Pro Pro Asn Ile  
 580 585 590

Cys Ile Val Thr Glu Tyr Cys Pro Arg Gly Ser Leu Gln Asp Ile Leu  
 595 600 605

Glu Asn Asp Ser Ile Asn Leu Asp Trp Met Phe Arg Tyr Ser Leu Ile  
 610 615 620

Asn Asp Leu Val Lys Gly Met Ala Phe Leu His Asn Ser Ile Ile Ser  
 625 630 635 640

Ser His Gly Ser Leu Lys Ser Ser Asn Cys Val Val Asp Ser Arg Phe  
 645 650 655

Val Leu Lys Ile Thr Asp Tyr Gly Leu Ala Ser Phe Arg Ser Thr Ala  
 660 665 670

Glu Pro Asp Asp Ser His Ala Leu Tyr Ala Lys Lys Leu Trp Thr Ala  
 675 680 685

Pro Glu Leu Leu Ser Gly Asn Pro Leu Pro Thr Thr Gly Met Gln Lys  
 690 695 700

Ala Asp Val Tyr Ser Phe Gly Ile Ile Leu Gln Glu Ile Ala Leu Arg  
 705 710 715 720

Ser Gly Pro Phe Tyr Leu Glu Gly Leu Asp Leu Ser Pro Lys Glu Ile  
 725 730 735

Val Gln Lys Val Arg Asn Gly Gln Arg Pro Tyr Phe Arg Pro Ser Ile  
 740 745 750

Asp Arg Thr Gln Leu Asn Glu Glu Leu Val Leu Leu Met Glu Arg Cys  
 755 760 765

Trp Ala Gln Asp Pro Ala Glu Arg Pro Asp Phe Gly Gln Ile Lys Gly  
 770 775 780

Phe Ile Arg Arg Phe Asn Lys Glu Gly Gly Thr Ser Ile Leu Asp Asn  
785 790 795 800  
  
Leu Leu Leu Arg Met Glu Gln Tyr Ala Asn Asn Leu Glu Lys Leu Val  
805 810 815  
  
Glu Glu Arg Thr Gln Ala Tyr Leu Glu Glu Lys Arg Lys Ala Glu Ala  
820 825 830  
  
Leu Leu Tyr Gln Ile Leu Pro His Ser Val Ala Glu Gln Leu Lys Arg  
835 840 845  
  
Gly Glu Thr Val Gln Ala Glu Ala Phe Asp Ser Val Thr Ile Tyr Phe  
850 855 860  
  
Ser Asp Ile Val Gly Phe Thr Ala Leu Ser Ala Glu Ser Thr Pro Met  
865 870 875 880  
  
Gln Val Val Thr Leu Leu Asn Asp Leu Tyr Thr Cys Phe Asp Ala Ile  
885 890 895  
  
Ile Asp Asn Phe Asp Val Tyr Lys Val Glu Thr Ile Gly Asp Ala Tyr  
900 905 910  
  
Met Val Val Ser Gly Leu Pro Gly Arg Asn Gly Gln Arg His Ala Pro  
915 920 925  
  
Glu Ile Ala Arg Met Ala Leu Ala Leu Leu Asp Ala Val Ser Ser Phe  
930 935 940  
  
Arg Ile Arg His Arg Pro His Asp Gln Leu Arg Leu Arg Ile Gly Val  
945 950 955 960  
  
His Thr Gly Pro Val Cys Ala Gly Val Val Gly Leu Lys Met Pro Arg  
965 970 975  
  
Tyr Cys Leu Phe Gly Asp Thr Val Asn Thr Ala Ser Arg Met Glu Ser  
980 985 990  
  
Asn Gly Gln Ala Leu Lys Ile His Val Ser Ser Thr Thr Lys Asp Ala  
995 1000 1005  
  
Leu Asp Glu Leu Gly Cys Phe Gln Leu Glu Leu Arg Gly Asp Val

1010		1015		1020
Glu Met Lys Gly Lys Gly Lys Met Arg Thr Tyr Trp Leu Leu Gly				
1025		1030		1035
Glu Arg Lys Gly Pro Pro Gly Leu Leu				
1040		1045		
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Met Pro Ser Leu Leu Val Leu Thr Phe Ser Pro Cys Val Leu Leu Gly				
1	5		10	15
Trp Ala Leu Leu Ala Gly Gly Thr Gly Gly Gly Gly Val Gly Gly Gly				
	20		25	30
Gly Gly Gly Ala Gly Ile Gly Gly Gly Arg Gln Glu Arg Glu Ala Leu				
	35		40	45
Pro Pro Gln Lys Ile Glu Val Leu Val Leu Leu Pro Gln Asp Asp Ser				
	50		55	60
Tyr Leu Phe Ser Leu Thr Arg Val Arg Pro Ala Ile Glu Tyr Ala Leu				
65		70	75	80
Arg Ser Val Glu Gly Asn Gly Thr Gly Arg Arg Leu Leu Pro Pro Gly				
	85		90	95
Thr Arg Phe Gln Val Ala Tyr Glu Asp Ser Asp Cys Gly Asn Arg Ala				
	100		105	110
Leu Phe Ser Leu Val Asp Arg Val Ala Ala Ala Arg Gly Ala Lys Pro				
	115		120	125
Asp Leu Ile Leu Gly Pro Val Cys Glu Tyr Ala Ala Ala Pro Val Ala				
	130		135	140
Arg Leu Ala Ser His Trp Asp Leu Pro Met Leu Ser Ala Gly Ala Leu				
145		150	155	160

Ala Ala Gly Phe Gln His Lys Asp Ser Glu Tyr Ser His Leu Thr Arg  
165 170 175

Val Ala Pro Ala Tyr Ala Lys Met Gly Glu Met Met Leu Ala Leu Phe  
180 185 190

Arg His His His Trp Ser Arg Ala Ala Leu Val Tyr Ser Asp Asp Lys  
195 200 205

Leu Glu Arg Asn Cys Tyr Phe Thr Leu Glu Gly Val His Glu Val Phe  
210 215 220

Gln Glu Glu Gly Leu His Thr Ser Ile Tyr Ser Phe Asp Glu Thr Lys  
225 230 235 240

Asp Leu Asp Leu Glu Asp Ile Val Arg Asn Ile Gln Ala Ser Glu Arg  
245 250 255

Val Val Ile Met Cys Ala Ser Ser Asp Thr Ile Arg Ser Ile Met Leu  
260 265 270

Val Ala His Arg His Gly Met Thr Ser Gly Asp Tyr Ala Phe Phe Asn  
275 280 285

Ile Glu Leu Phe Asn Ser Ser Ser Tyr Gly Asp Gly Ser Trp Lys Arg  
290 295 300

Gly Asp Lys His Asp Phe Glu Ala Lys Gln Ala Tyr Ser Ser Leu Gln  
305 310 315 320

Thr Val Thr Leu Leu Arg Thr Val Lys Pro Glu Phe Glu Lys Phe Ser  
325 330 335

Met Glu Val Lys Ser Ser Val Glu Lys Gln Gly Leu Asn Met Glu Asp  
340 345 350

Tyr Val Asn Met Phe Val Glu Gly Phe His Asp Ala Ile Leu Leu Tyr  
355 360 365

Val Leu Ala Leu His Glu Val Leu Arg Ala Gly Tyr Ser Lys Lys Asp  
370 375 380

Gly Gly Lys Ile Ile Gln Gln Thr Trp Asn Arg Thr Phe Glu Gly Ile  
 385 390 395 400

Ala Gly Gln Val Ser Ile Asp Ala Asn Gly Asp Arg Tyr Gly Asp Phe  
 405 410 415

Ser Val Ile Ala Met Thr Asp Val Glu Ala Gly Thr Gln Glu Val Ile  
 420 425 430

Gly Asp Tyr Phe Gly Lys Glu Gly Arg Phe Glu Met Arg Pro Asn Val  
 435 440 445

Lys Tyr Pro Trp Gly Pro Leu Lys Leu Arg Ile Asp Glu Asn Arg Ile  
 450 455 460

Val Glu His Thr Asn Ser Ser Pro Cys Lys Ser Ser Gly Gly Leu Glu  
 465 470 475 480

Glu Ser Ala Val Thr Gly Ile Val Val Gly Ala Leu Leu Gly Ala Gly  
 485 490 495

Leu Leu Met Ala Phe Tyr Phe Phe Arg Lys Lys Tyr Arg Ile Thr Ile  
 500 505 510

Glu Arg Arg Thr Gln Gln Glu Glu Ser Asn Leu Gly Lys His Arg Glu  
 515 520 525

Leu Arg Glu Asp Ser Ile Arg Ser His Phe Ser Val Ala  
 530 535 540